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Nov 6 2006 15:24:20

## Appendix

Site-specific recombinase [*Streptococcus pyogenes*], plasmid pSM19035

Accession YP\_232767.1 GI:63021996

makigyarvsskeqnldrqlqalqgvsksdklsgqsverpqlqamlnyiregddivvteldrlgrnnkeltelmnaiqqkgatlevlnlpsmngie  
denlrrlinnlvielykyqaeserkrikerqaqgieiaxskgkfkgrqhkfendprkhafdlflngcsdkeveeqtginrrtfrrytrytrnvtvdqrknk  
gkrds

		Score (Bits)	E Value
A partial list of sequences producing significant alignments			
gi 63021985 ref YP_232754.1  site-specific recombinase [Strep...	316	3e-85	
gi 81176607 gb ABB59535.1  putative resolvase [Pediococcus acidi	305	7e-82	
gi 10956207 ref NP_044464.1  resolvase [Streptococcus agalact...	302	8e-81	
gi 392559 gb AAA73395.1  resolvase protein [Streptococcus agalac	301	1e-80	
gi 6690329 gb AAF24086.1 AF117258_3 resolvase [Staphylococcus au	297	2e-79	
gi 3023049 gb AAC38605.1  resolvase [Enterococcus faecalis]	293	4e-78	
gi 6746431 gb AAF27558.1  putative resolvase [Lactococcus lactis	254	1e-66	
gi 6739586 gb AAF27319.1  putative resolvase [Lactococcus lactis	251	1e-65	
gi 58701072 gb AAW81284.1  hypothetical protein [Lactobacillus p	236	3e-61	
gi 108736165 gb ABG00294.1  ORF12 [Lactococcus lactis]	236	4e-61	
gi 116334884 ref YP_796409.1  Site-specific recombinase, DNA ...	235	1e-60	
gi 56707177 ref YP_163807.1  putative resolvase [Lactobacillu...	234	2e-60	
gi 75181775 gb ABA12807.1  hypothetical protein [Lactobacillus p	233	3e-60	
gi 75182232 gb ABA12841.1  conserved hypothetical protein [La...	233	4e-60	
gi 5420101 emb CAB46556.1  putative resolvase [Streptococcus the	231	2e-59	
gi 29377950 ref NP_817076.1  site-specific recombinase, resol...	216	5e-55	
gi 69247432 ref ZP_00604345.1  recombinase Sin [Enterococcus ...	185	1e-45	
gi 116326678 ref YP_796452.1  Site-specific recombinase, DNA ...	156	6e-37	
gi 116490744 ref YP_810288.1  Site-specific recombinase, DNA ...	134	2e-30	
gi 69247633 ref ZP_00604427.1  Resolvase, N-terminal:Resolvas...	133	4e-30	
gi 69250457 ref ZP_00605155.1  Resolvase, N-terminal [Enteroc...	129	8e-29	
gi 81330302 ref YP_398694.1  hypothetical protein pHbeta_52 ...	127	4e-28	
gi 116493435 ref YP_805170.1  Site-specific recombinase, DNA ...	119	7e-26	
gi 37595767 ref NP_932185.1  Res2 [Staphylococcus aureus] >gi...	117	2e-25	
gi 82743151 ref ZP_00905814.1  integrative genetic element Gs...	115	1e-24	
gi 495089 gb AAA26675.1  recombinase >gi 8574415 emb CAB94806...	115	2e-24	
gi 1086524 gb AAB08926.1  invertase-enterococcal	113	4e-24	
gi 82751033 ref YP_416774.1  recombinase [Staphylococcus aure...	112	1e-23	
gi 22476843 gb AAM97333.1 AF426833_2 recombinase Sin [Staphyloco	111	2e-23	
gi 13793990 gb AAK38455.1  recombinase Sin [Staphylococcus epide	110	3e-23	
gi 22476850 gb AAM97339.1 AF426834_5 recombinase Sin [Staphyloco	110	5e-23	
gi 70727309 ref YP_254225.1  recombinase Sin [Staphylococcus ...	109	6e-23	
gi 11230707 emb CAC16669.1  recombinase [Staphylococcus haemolyt	109	9e-23	
gi 8980455 emb CAB96927.1  Bin3 protein [Stenotrophomonas maltop	108	2e-22	
gi 38257108 ref NP_940770.1  recombinase [Staphylococcus warn...	107	3e-22	
gi 116514884 ref YP_813790.1  Site-specific recombinase, DNA ...	107	5e-22	
gi 111017138 ref YP_700110.1  possible resolvase, N-terminal ...	106	6e-22	
gi 11968214 ref NP_072000.1  recombinase [Enterococcus faecal...	105	1e-21	
gi 110628945 gb ABG79938.1  resolvase [Lactobacillus reuteri]	104	2e-21	
gi 32455946 ref NP_862404.1  putative transposon resolvase [M...	104	3e-21	

Application/Control Number: 10/808,161

Art Unit: 1633

### Example Alignment

gi|116326678|ref|YP\_796452.1| Site-specific recombinase, DNA invertase Pin related protein, [Lactobacillus casei ATCC 334]

gi|116106496|gb|ABJ71637.1| Site-specific recombinase, DNA invertase Pin related protein, [Lactobacillus casei ATCC 334]

Score = 156 bits (394), Expect = 6e-37, Method: Composition-based stats.  
Identities = 88/156 (56%), Positives = 121/156 (77%), Gaps = 2/156 (1%)

Query 1 MAKIGYARVSSKEQNLDRQLQALQ--GVSKVFSDKLSGQSVERPQLQAMLNYIREGDIVV 58  
M+KIGYARVS+++QNL RQ++ L GV+K+F +KLSG++ +RPQL+AML+YIR+ D VV  
Sbjct 1 MSKIGYARVSTRDQNLARQIEQLHDAGVNKIFQEKGKNA DRPQLKAMLDYIRDDEVV 60

Query 59 VTELDRLGRNNKELTELMNAIQQQKGATLEVNLPSMNGIEDENLRRILINNLVIELKYQA 118  
V LDRLGRN+ +LT+++ I+ +GA L VLNLPs IED NLR LI +++ELYKY A  
Sbjct 61 VLSLDRLGRNSHDLTDIIETIRHRAQLNVNLPSFASTIEDPNLRLNLITTIIVELYKYIA 120

Query 119 ESERKRIKERQAQGIEIAKSKGKFGRQHKFKENDP 154  
+ ER+ IK RQ QGIEIAK +GK+KG+ ++ + P  
Sbjct 121 QEERETIKIRQQQGIEIAKRQGKYKGKIREYGP HSP 156